FIGURE 1

	ATGGGTTCCATGCGTCTATT 20
	M G S M R L L
prx	9+>
AGTAGTGGCATTGTTGTGCATTTGCTATGCATGCAG	GTTTTTCAGTCTCTTATGCTCA 80
V V A L L C A F A M H A	GFSVSYAQ 1
signal sequence	
	TCTTCCCTATTGTGTTTGGAGT 140
GCTTACTCCTACGTTCTACAGAGAAACATGTCCAAATC	L F P I V F G V 21
T T D T F Y K F 1 C F 14	
prx12+>	CCACTCTCATCAGGCTTCATTT 200
AATCTTCGATGCTTCTTTCACCGATCCCCGAATCGGGG	CCAGTCTCATGAGGCTTCATT 200 A S L M R L H F 41
IFDASFTDPRI <u>G</u>	A S L M R L H F 41 active site
I	<
TCATGATTGCTTTGTTCAAG GTTGTGATGGATCAGT	TTTGCTGAACAACACTGATACAAT 260
H D C F V Q G C D G S V	LLNNTDTI 61
prx10 prx2+ AGAAAGCGAGCAAGATGCACTTCCAAATATCAACTCAA	> \TAAGAGGATTGGACGTTGTCAA 320
	IRGLDVVN 81
ESEQDA 1	
TGACATCAAGACAGCGGTGGAAAATAGTTGTCCAGAC	ACAGTTTCTTGTGCTGATATTCT 380
DIKTAVENSCPD	T V S C A D I L 101
II	
TGCTATTGCAGCTGAAATAGCTTCTGTTCTG GGAGG.	AGGTCCAGGATGGCCAGTTCCATT 440
A I A A E I A S V L G G	G P G W P V P L 121
	CCXXXTCXXXXCCTTCCAGCACC 500
AGGAAGAAGGGACAGCTTAACAGCAAACCGAACCCTT	A N O N L P A P 141
GRRDSLTANRTL	
TTTCTTCAACCTCACTCAACTTAAAGCTTCCTTTGCT	GTTCAAGGTCTCAACACCCTTGA 560
FFNLTQLKASFA	V Q G L N T L D 161
III TTTAGTTACACTCTCAG GTGGTCATACGTTTGGAAG	AGCTCGGTGCAGTACATTCATAAA 620
TTTAGTTACACTCTCAG GIGGTCATTGGTTACACTCTCAG GIGGTCATTTACACTCTCAG GIGGTCATTCAG GIGGTCATTACACTCTCAG GIGGTCATTTACACTCTCAG GIGGTCATTACACTCTCAG GIGGTCAACTCTCAG GIGGTCATTACACTCTCAG GIGGTCATTACACTCTCAG GIGGTCATTACACTCACACTCTCAACTCTCAACTCTCAACTCTCAACTCTCAACTCTCAACTCTCAACTCTCAACTCTCAACTCAACTCTCAACTCTCAACTCAACTCAACTCTCAACTCTCAACTCAACTCAACTCTCAACTCAACTCTCAACAA	ARCSTFIN 181
heme-binding domain	
CCGATTATACAACTTCAGCAACACTGGAAACCCTGAT	CCAACTCTGAACACAACATACTT 680
	PTLNTTYL 201
R L Y N F S N I S II -	
AGAAGTATTGCGTGCAAGATGCCCCCAGAATGCAACT	GGGGGATAACCTCACCAATTTGGA 741
E V L R A R C P Q N A T	G D N L T N L D 22
	TTCCAATCTTCTGCAGCTCAATGG 80
CCTGAGCACACCTGATCAATTTGACAACAGATACTAC	S N L L Q L N G 24
L S T P D Q F D M M -	
CTTA CTTCAGAGTGACCAAGAACTTTTCTCCACTCC	GGTGCTGATACCATTCCCATTGT 86

L	L	Q	S	D	Q	E	L	F	S	T	P	G	A	D	T	I	P	I	V	261
							<			prx	:6 -									•
CAAT	'AGC	ጥጥር	AGC	'AGT	'AAC	CAG									GTT	TCA	ATG	ATA	AA	920
N	S	F	S	S	N	Q	N			F			F		V		M		K	281
AATG	GGT	'AAT	'ATT	'GGA	.GTG	CTG	ACT	'GGG	GAT	'GAA	.GGA	GAA	ATT	'CGC	TTG	CAA	TGT	'AAT	'TT	980
M	G	N		G		L		G		E		E		R	L	Q	С	N	F	301
TGTG	LAA	'GGA	.GAC	TCG	TTT	GGA	ATT.	GCT	'AGT	'GTG	GCG	TCC	'AAA	GAT	'GCT	'AAA	.CAA	AAG	CT	1040
V	N	G	D	S	F	G	L	A	S	V	A	S	K	D	A	K	Q	K	L	321
TGTI V	GCT A	'CAA Q		'AAA K	TAA *	ACC	ZAAT	TAA'	'TAA	TGG	IGGA	TGT	'GCA	TGC	TAG	CTA	.GCA	TGT	'AA	1100 326
AGGC	'AAA	ATT.	.GGT	TGT	'AAA'	.CCT	'CTT	'TGC	'TAG	CTA	LAT	TGA	TAA	'AAA	CCA	AAG	GAG	TAG	TG	1160
TGCA	TGT	'CAA	TTC	GAI	TTT	'GCC	ATG	TAC	CTC	TTG	GAA	TAT	'TAT	'GTA	ATA	ATI	'ATT	TGA	AT	1220
רידניז	מייייי	AGG	TAC	TTA	ATT	'AA'	'C (A	l) n												

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FIGURE 2

60 40 50 30 20 10 1 GCATCATATCATAAACAATACGTACGTGATATTATCTAGTGTCTCTCAGTTTACTTTATG 121 CAAGAAATCCGCCGAATTCATCTCTATAAATAAAAGGATCTATATGAGAGGTAAAATCAT 181 ATTAACTCAAAATGGGTTCCATGCGTCTATTAGTAGTGGCATTGTTGTGTGCATTTGCTA 241 TGCATGCAGGTTTTTCAGTCTCTTATGCTCAGCTTACTCCTACGTTCTACAGAGAAACAT 301 GTCCAAATCTGTTCCCTATTGTGTTTTGGAGTAATCTTCGATGCTTCTTTCACCGATCCCC 421 TTTTTTTCCTTCCAAAATGCCCTGCATATTTAACAAGATTGCTTTGTTCACCTAGAAAA 541 GATCAAGAAAATAGCTAGAAAGAAAGCAACGTTTTTTTAAAAAGGTATTTAGTGTGAGAAA 601 AATATTAAAACTGAAGAGAAAGAAATTAAATAAGCTTTTCTTGAATGATATTTACATGTC 661 TTATTAACTTAAAGTCACCTTTTTTCTTTAAGTTGTGCTTGAAGAAAAAAGATGTCTTTC 781 TTTACCATATTATTACTATATTTCATGATGACAACAGACAAGTATTCTAAAGAGGT 841 ATCGGTAGATGATTAATTTTTTTATAAAAAAATCTTTTGCGTGTATAGATATTCTTTTAT 901 AATTGGTGCAGAAACTTGTAATGCTAATTGCAATTAATCTTACATTGATTAACTAATAGC 961 TATAATCAATATTTAGGTTAGGTATAGGAGACAAATCAAGTGATCTGAACAAATTAAGTT 1021 GTTATATTTGCATTGTGACAGGGTTGTGATGGATCAGTTTTGCTGAACAACACTGATACA 1081 ATAGAAAGCGAGCAAGATGCACTTCCAAATATCAACTCAATAAGAGGATTGGACGTTGTC 1141 AATGACATCAAGACAGCGGTGGAAAATAGTTGTCCAGACACAGTTTCTTGTGCTGATATT 1261 AACCATTAAAAAGTTGCATGATTGGATTCAAAATTCTATGGTATTGGGGTTCTGATATAA 1501 GGATGGAATCAGTCAAAACATTTAATTCAAAATACTCTTAATTGTGATTAGTAATCATGT 1621 GCAAGCCGGTTGGTATAGATATCACTGGCCTGTAGAATATGTGGTTTTTCACGTTTAAAT 1741 TATTGACTGTGAAACATGTTTCCACACACAGGCTTAGAAACTCCTCGCAACTAACATCTC 1801 CAAAATTTGACTATTTATTATGAAGATAATTCATCTATGATGTTCAACTCTATTATATA 1861 TATGTATCATCGCAGTATTAAGAATTATAATAGTCAAATATAGAAGTATATCGGGTAAAT 1981 GAAAATAACGATGAACTAAAAACGAAAGGGTATCATATAGTTTGACTTTTATGTTAGAGA 2041 GAGACATCTTAATTTGGTCATATGTTAAATAATTAATTACAATGCATACACAAATATTTA 2101 TGCCATATCTAAAAAATGATAAAATATCATAGGTATACTCAACTATATGATATCCCCATA 2221 ATCCACTTAAAGTGGTTCAACATATTTATGTAATAATTTACAGGGAGGAGGTCCAGGATG 2281 GCCAGTTCCATTAGGAAGAAGGGACAGCTTAACAGCAAACCGAACCCTTGCAAATCAAAA 2341 CCTTCCAGCACCTTTCTTCAACCTCACTCAACTTAAAGCTTCCTTTGCTGTTCAAGGTCT 2521 TTTATAATAAAATTATCAATTTATGTACTTAAAAAATTATGGATTGAAGCTCTTTTCATCC 2581 AACTTTTACTAAAGTTAAGGTGCATATAATATAAAATAAACTATCTCTTGTTTCTTATAA 2641 AAAGATTGAAGATAAGTTAAAGTCTACTTATAAATCATTAATATATGTATAGGTGGTCAT 2701 ACGTTTGGAAGAGCTCGGTGCAGTACATTCATAAACCGATTATACAACTTCAGCAACACT 2761 GGAAACCCTGATCCAACTCTGAACACATACTTAGAAGTATTGCGTGCAAGATGCCCC 2821 CAGAATGCAACTGGGGATAACCTCACCAATTTGGACCTGAGCACACCTGATCAATTTGAC 2881 AACAGATACTACTCCAATCTTCTGCAGCTCAATGGCTTACTTCAGAGTGACCAAGAACTT 2941 TTCTCCACTCCTGGTGCTGATACCATTCCCATTGTCAATAGCTTCAGCAGTAACCAGAAT 3001 ACTTTCTTTTCCAACTTTAGAGTTTCAATGATAAAAATGGGTAATATTGGAGTGCTGACT

FIGURE 3A

L78163	ATGGGTTCCATGCGT-CTATTAGTAGTGGCATTGTTG	36
U41657		0
X90693	GGCAAA-CAATGAACTCCCTTCGTGCTGTAGCAATAG-CTTTGTGC	44
X90694	GCTCTTCAAAACAATGAACTCCTTAGCAACTT-CTATGTGG	40
L36156	TTAGCAACTT-CTATGTGG	22
X90692	AATGCTTGGTCTAAGTGCAACAGCTTTTTGCTGTATGG	38
L78163	TGTGCATTT-GCTATGCATGCAGGTTTTTCAGTCTCTTATGC	77
U41657		0
X90693	TGTATTGTGGTTGTGCTTGGAGGGTTACCCTTCTCTCAAATGC	88
X90694	TGTGTTGTGCTTTAGTTGTGCTTGGAGGACTACCCTTTTCCTCAGATGC	90
L36156	TGTGTTGTGCTTTAGTTGTGCTTGGAGGACTACCCTTTTCCTCAGATGC	72
X90692	TGT-TTGTGCTAATTGGAGGAGTACCCTTTTCAAATGC	75
L78163	TCAGCTTACTCCTACGTTCTACAGAGAAACATGTCCAAATCTGTTCCCTA	127
U41657		0
X90693	GCAACTTGATCCATCCTTTTACAGGAACACTTGTCCAAATGTTAGTTCCA	138
X90694	ACAACTTAGTCCCACTTTTTACAGCAAAACGTGTCCAACTGTTAGTTCCA	140
L36156	ACAACTTAGTCCCACTTTTTACAGCAAAACGTGTCCAACTGTTAGTTCCA	122
X90692	ACAACTAGATCCTTCATTTTACAACAGTACATGTTCTAATCTTGATTCAA	125
A90692	ACMCIndia Contract	
L78163	TTGTGTTTGGAGTAATCTTCGATGCTTCTTTCACCGATCCCCGAATCGGG	177
U41657		0
X90693	TTGTTCGTGAAGTCATAAGGAGTGTTTCTAAGAAAGATCCTCGTATGCTT	188
X90694	TTGTTAGCAATGTCTTAACAAACGTTTCTAAGACAGATCCTCGCATGCTT	190
L36156	TTGTTAGCAATGTCTTAACAAACGTTTCTAAGACAGATCCTCGCATGCTT	172
X90692	TCGTACGTGGTGTCTCACAAATGTTTCACAATCTGATCCCAGAATGCTT	175
L78163	GCCAGTCTCATGAGGCTTCATTTTCATGATTGCTTTGTTCAAGGTTGTGA	227
U41657	TTTCATGATTGCTTTGTTCAAGGTTGTGA	29
X90693	GCTAGTCTTGTCAGGCTTCACTTTCATGACTGTTTTGTTCAAGGTTGTGA	238
X90694	GCTAGTCTCGTCAGGCTTCACTTTCATGACTGTTTTGTTCTGGGATGTGA	240
L36156	GCTAGTCTCGTCAGGCTTCACTTTCATGACTGTTTTTGTTCTGGGATGTGA	222
X90692	GGTAGTCTCATCAGGCTACATTTTCATGACTGTTTTGTTCAAGGTTGCGA	225
K90092	**********	
L78163	TGGATCAGTTTTGCTGAACAACACTGATACAATAGAAAGCGAGCAAGATG	277
U41657	TGGATCAGTTTTACTGAACAACACTGATACAATAGAAAGCGAGCAAGATG	79
X90693	TGCATCAGTTTTACTAAACAAAACTGATACCGTTGTGAGTGA	288
X90694	TGCCTCAGTTTTGCTGAACAATACTGCTACAATCGTAAGCGAACAACAAG	290
L36156	TGCCTCAGTTTTGCTGAACAATACTGCTACAATCGTAAGCGAACAACAAG	272
X90692	TGCCTCGATTTTGCTGAACGATACGGCTACAATAGTGAGCGAGC	275
1150052	** ** *** *** ** ** ** * ** * * * * * *	
L78163	CACTTCCAAATATCAACTCAATAAGAGGATTGGACGTTGTCAATGACATC	327
U41657	CACTTCCAAATATCAACTCAATAAGAGGATTGGACGTTGTCAATGACATC	129
X90693	CTTTTCCAAACAGAAACTCATTAAGAGGTTTGGATGTTGTGAATCAAATC	338
X90693 X90694	CTTTTCCAAATAACAACTCTCTAAGAGGTTTGGATGTTGTGAATCAGATC	340
L36156	CTTTTCCAAATAACAACTCTCTAAGGGGTTTGGATGTTGTGAATCAGATC	322
	CACCACCAAATAACAACTCCATAAGAGGTTTGGATGTGATAAACCAGATC	325
X90692	***** *. **** **.** **** **. * ***	
L78163	AAGACAGCGGTGGAAAATAGTTGTCCAGACACAGTTTCTTGTGCTGATAT	377

U41657	AAGACAGCGGTGGAAAATAGTTGTCCAGACACAGTTTCTTGTGCTGATAT	179
X90693	AAAACAGCTGTGGAAAAGGCTTGTCCTAACACAGTTTCTTGTGCTGATAT	388
X90694	AAACTGGCTGTAGAAGTGCCTTGTCCTAACACAGTTTCTTGTGCTGATAT	390
L36156	AAAACTGCTGTAGAAAGTGCTTGTCCTAACACAGTTTCTTGTGCTGATAT	372
X90692	AAAACAGCGGTGGAAAATGCTTGTCCTAACACAGTTTCTTGTGCTGATAT	375
	**	
L78163	TCTTGCTATTGCAGCTGAAATAGCTTCTGTT-CTGGGAGGAGGTCCAGGA	426
U41657	TCTTGCTATTGCAGCTGAAATAGCTTCTGTTGCTGGGAGGAGGTC-AGGA	228
X90693	TCTTGCTCTTTCTGCTGAATTATCATCTACA-CTGGCAGATGGTCCTGAC	437
X90694	TCTTGCACTTGCTCCAAGCATCCTCTGTT-CTGGCACAAGGTCCTAGT	439
L36156	TCTTGCACTTGCTCAAGCATCCTCTGTT-CTGGCACAAGGTCCTAGT	418
X90692	TCTTGCTCTTTCTGCTGAAATATCATCTGAT-CTGGCAAATGGTCCTACT	424
A90092	******	723

L78163	TGGCCAGTTCCATTAGGAAGAAGGGACAGCTTAACAGCAAACCGAACCCT	476
U41657	TGGCCAGTTCCATTAGGAAGAAGGGACAGCTTAACAGCAAACCGAACCCT	278
X90693	TGGAAGGTTCCTTTAGGAAGAAGAGATGGTTTAACGGCAAACCAGTTACT	487
X90694	TGGACGGTTCCTTTAGGAAGAAGGGATGGTTTAACCGCAAACCGAACACT	489
L36156	TGGACGGTTCCTTTAGGAAGAAGGGATGGTTTAACCGCAAACCGAACACT	468
X90692	TGGCAAGTTCCATTAGGAAGAAGGGATAGTTTGACAGCAAATAATTCCCT	474
N90092	***	1 · 1
L78163	TGCAAATCAAAACCTTCCAGCACCTTTCTTCAACCTCA-CTCAACTTA	523
U41657	TGCAAATCAAAACCTTCCAGCACCTTTCTTCAACCTCA-CTCAACTTA	325
X90693	TGCTAATCAAAATCTTCCAGCTCCTTTCAATACTACTGATCAACTTA	534
X90694	TGCAAATCAAAATCTTCCGGCTCCATTCAATTCCTTGGATCAACTTA	536
L36156	TGCAAATCAAAATCTTCCGGCTCCATTCAATTCCTTGGATCACCTTA	515
X90692	TGCAGCTCAAAATCTTCCTGCCCCCACTTTCAACCTTA-CTCGACTAA	521
112 002 1	***	
L78163	AAGCTTCCTTTG-CTGTTCAAGGTCTCAACACCCTTGATTTAGTTACACT	572
U41657	AAGCTTCCTTTG-CTGTTCAAGGTCTCAACACCCTTGATTTAGTTACACT	374
X90693	AAGCTGCATTTG-CTGCTCAAGGTCTCGATACTACTGATCTGGTTGCACT	583
X90694	AAGCTGCATTT-ACTGCTCAAGGCCTCAATACTACTGATCTAGTTGCACT	585
L36156	AA-CTGCATTTGACTGCTCAAGGCCTCATTACTCCTGTTCTAGTTGCCCT	564
X90692	AATCTAACTTTGA-TAATCAAAACCTCAGTACTACTGATCTAGTTGCACT	570
	** **. *** *. ****. ** **. ** * * **. * **	
L78163	CTCAGGTGGTCATACGTTTGGAAGAGCTCGGTGCAGTACATTCATAAACC	622
U41657	CTCAGGTGGTCATACGTCTGGAAGAGCTCGGTGCAGTACATTCATAAACC	424
X90693	CTCCGGTGCTCATACATTTGGAAGAGCTCATTGCTCTTTATTTGTTAGCC	633
X90694	CTCGGGTGCTCATACATTTGGAAGAGCTCATTGCGCACAATTTGTTAGTC	635
L36156	CTCGGGTGCTCATACATTTGGAAGAGCTCATTGCGCACAATTTGTTAGTC	614
X90692	CTCAGGTGGCCATACAATTGGAAGAGGTCAATGCAGATTTTTCGTTGATC	620
· -	*** **** ***** ****** **	
L78163	GATTATACAACTTCAGCAACACTGGAAACCCTGATCCAACTCTGAACACA	672

GATTATACAACTTCAGCAACACTGGA----CTGATCCA-CT-TGGACACA

468

U41657

X90693	GATTGTACAACTTCAGCGGTACGGGAAGTCCCGATCCAACTCTTAACACA	683
X90694	GATTGTACAACTTCAGCAGTACTGGAAGTCCCGATCCAACTCTTAACACA	685
L36156	GATTGTACAACTTCAGCAGTACTGGAAGTCCCGATCCAACTCTTAACACA	664
X90692	GATTATACAATTTCAGCAACACTGGAAACCCCGATTCAACTCTTAACACG	670
	**** * * * * * * * * * * * * * * * * * *	
L78163	ACATACTTAGAAGTATTGCGTGCAAGATGCCCCCAGAATGCAACTGGGGA	722
U41657	ACATACTTAGAAGTATTGCGTGCAAGATGCCCCCAGAATGCAACTGGGGA	518
X90693	ACTTACTTACAACAATTGCGCACAATATGTCCCAATGGTGGACCTGGCAC	733
X90694	ACTTACTTACAACAACTGCGCACAATATGTCCCAATGGTGGACCTGGCAC	735
L36156	ACTTACTTACAACAACTGCGCACAATATGTCCCAATGGTGGACCTGGCAC	714
X90692	ACCTATTTACAAACATTGCAAGCAATATGTCCCAATGGTGGACCTGGTAC	720
	** ** *** ** * *** . *** *** *** *	
L78163	TAACCTCACCAATTTGGACCTGAGCACACCTGATCAATTTGACAACAGAT	772
U41657	TAACCTCACCAATTTGGACCTGAGCACACCTGATCAATTTGACAACAGAT	568
X90693	GAACCTTACCAATTTCGATCCAACGACTCCTGATAAATTTGACAAGAACT	783
X90694	AAACCTTACCAATTTCGATCCAACGACTCCTGATAAATTTGACAAGAACT	785
L36156	AAACCTTACCAATTTCGATCCAACGACTCCTGATAAATTTGACAAGAACT	764
X90692	AAACCTAACCGATTTGGACCCAACCACACCAGATACATTTGACTCCAACT	770
	·**** *** *** ** * · * · ** · ** · **	
L78163	ACTACTCCAATCTTCTGCAGCTCAATGGCTTACTTCAGAGTGACCAAGAA	822
U41657	ACTACTCCAATCTTCTGCAGCTCAATGGCTTACTTCAGAGTGACCAAGAA	618
X90693	ATTACTCTAATCTTCAAGTGAAAAAAGGTTTGCTTCAAAGTGATCAAGAG	833
X90694	ATTACTCCAATCTTCAAGTGAAAAAGGGTTTGCTCCAAAGTGATCAAGAG	835
L36156	ATTACTCCAATCTTCAAGTGAAAAAGGGTTTGCTCCAAAGTGATCAAGAG	814
X90692	ACTACTCCAATCTCCAAGTTGGAAAGGGCTTGTTTCAGAGTGACCAAGAG	820
	* **** **** * ** . * * * * * *	
L78163	CTTTTCTCCACTCCTGGTGCTGATACCATTCCCATTGTCAATAGCTTCAG	872
U41657	CGTTTCTCCACTCCTGGTGCTGATACCATTCC-ATTGTCAATAGCTTCAG	667
X90693	TTGTTCTCAACATCTGGTTCAGATACCATTAGCATTGTCAACAAATTCGC	883
X90694	TTGTTCTCAACTTCTGGTGCAGATACCATTAGCATTGTCAACAAATTCAG	885
L36156	TTGTTCTCAACTTCTGGTGCAGATACCATTAGCATTGTCGACAAATTCAG	864
X90692	CTTTTTTCCAGAAATGGTTCTGACACTATTTCTATTGTCAATAGTTTCGC	870
	** ** * . ****.*.** *** ****.* *. ***.	
L78163	CAGTAACCAGAATACTTTCTTTTCCAACTTTAGAGTTTCAATGATAAAAA	922
U41657	CGAACCAGAATACTTTCTTTTCCAACTTTAGAGTTTCAATGATAAAAA	715
X90693	AACCGATCAAAAAGCTTTTTTTGAGAGCTTTAGGGCTGCTATGATCAAAA	933
X90694	CACCGATCAAAATGCTTTCTTTGAGAGCTTTAAGGCTGCAATGATTAAAA	935
L36156	CACCGATCAAAATGCTTTCTTTGAGAGCTTTAAGGCTGCAATGATTAAAA	914
X90692	CAATAATCAAACTCTCTTCTTTGAAAATTTTTGTAGCCTCAATGATAAAAA	920
	* * * * * * * * * * * * * * * * * *	
L78163	TGGGTAATATTGGAGTGCTGACTGGGGATGAAGGAGAAATTCGCTTGCAA	972
U41657	TGGGTAATATTGGAGTGCTGACTGGGGATGAAGGAGAAATTCGCTTGCAA	765
X90693	TGGGAAATATTGGTGTTAACCGGGAACCAAGGAGAGATTAGAAAACAA	983
X90694	TGGGCAATATTGGTGTGCTAACAGGGACAAAAGGAGAGATTAGAAAACAA	985
L36156	TGGGCAATATTGGTGTGCTAACAGGGACAAAAGGAGAGATTAGAAAACAA	964
X90692	TGGGTAATATTGGAGTTTTAACTGGATCTCAAGGTGAAATTAGAACACAG	970

	**** ******* * * * * * * * * * * * * * *	
L78163	TGTAATTTTGTGAATGGAGACTCGTTTGGATTAGC	1007
U41657	TGTAATTTTGTGAATGGAGACTCGTTTGGATTAGC	800
X90693	TGCAACTTTGTTAATTCAAAATCAGCAGAACTTGGTCTTAT	1024
X90694	TGCAACTTTGTGAACTTTGTGAACTCAAATTCTGCAGAACTAGATTTAGC	1035
L36156	TGCAACTTTGTGAACTCAAATTCTGCAGAACTAGATTTAGC	1005
X90692	TGTAATGCTGTGAATGGGAATTCTTCTGGATTGGC	1005
	** . *	
L78163	TAGTGTGGCGTCCAAAGATGCTAAACAAAAGCTTGTTGCTCAATCTAAAT	1057
U41657	TAGTGTGGCGTCCAAAGATGCTAAACAAAAGCTTGTTGCTCAATCTAAAT	850
X90693	CAATGTTGCCTCAGCAGATTCATCTG-AGGAGGGTATGGTTAG	1066
X90694	CACCATAGCATCCATAGTAGAATCATTAG-AGGATGGTATTGCTAGTG	1082
L36156	CACCATAGCATCCATAGTAGAATCATTAG-AGGATGGAATTGCTAGTG	1052
X90692	TACTGTAGTCACCAAAGAATCATCAG-AAGATGGAATGGCTAGCT	1049
	* .*.* .* .*** **	
L78163	AAACCAATAATTAATGGGGATGTGCATGCTAGCTAGCATGTAAAGGCAAA	1107
U41657	AAACCAATAATTAATGGGGATGTCGATGCTAGCTACGATGTAAAGGCAAA	900
X90693	CTCAATGTAAA-TG-TAG	1082
X90694	TAATATAAATAAATTAGCGTAAATGCACTTATTGAA-ATCTTG	1124
L36156	TAATATAAATAAATTAGCGAAAATGCACTTATTGAA-ATCTTG	1094
X90692	CATTCTAAATATAAGCTTGGAAAATATTGAAGAGGTTCTAT	1090
	*	
L78163	TTAGGTTGTAAACCTCTTTGCTAGCTATATTGAAATAAACCAAAGGAGTA	1157
U41657	TTAGGTTG-AAACCTCTTTGCTAGCTATATTGAAATAAACCAAAGGAGTA	949
X90693	TGATTGGAAGCAACTAATAAATTAAGAAGCTATAACT	1119
X90694	TGACTAGATGCCACTAATAAATAAGTTATAACT	1157
L36156	TGACTAGATCCCACTAATAAATAAGTTATAACT	1127
X90692	AATTTTGTGCATACATATATGGTATGTG	1118
	* ** **	
L78163	GTGTGCATGTCAATTCGATTTTGC-CATGTACCTCTTGGAATAT	1200
U41657	GTGTCGATGTCAATTCGATTTTGC-CATGTACCTCTTGGAATATTATGTA	998
X90693	. ATGCACATT-CATGGTATGTGTGAGATAGTTATTAGATGCTTTGTGAGCA	1168
X90694	AGGCACATTTCATGTCACTTGAAATTTCATGCCT-GTATATGAG	1200
L36156	AGGCACATTTCATGTCACTTGAAATCCTATGCCTTGTATATTAGAGGACG	1177
X90692	CATGTGGTGTATTATGTTTTTGTTATGTTCTTCAAGTTGATCA	1161
	**	
L78163	1200	
U41657	ATAATTATTTGAATCTCAAAAAAAAAAAAAAA 1031	
X90693	AAAATCTTTTGGATTTCATTTGAAGTGTTTCT 1200	
X90694	1200	
L36156	TGT-TCTTCTTGGTATTATACTAT 1200	
X90692	GGGA-CTGTAGAAGCTCCCTAATAATATTTGTGTCAAAGT 1200	

FIGURE 3B

L78163	MGSMRLLVVALLCAFAMHAGFSVSYAQLTPTFYRETCPNLFPIVFGV	47
U41657		0
X90693 .	MNSLRAVAIALCCIVVVLGGLPFSSNAQLDPSFYRNTCPNVSSIVREV	48
X90694	MNSLATSMWCVVLLVVLGGLPFSSDAQLSPTFYSKTCPTVSSIVSNV	47
L36156	MWCVVLLVVLGGLPFSSDAQLSPTFYSKTCPTVSSIVSNV	40
X90692	MLGLSATAFCCMVFVLIGGVPFS-NAQLDPSFYNSTCSNLDSIVRGV	46
	IFDASFTDPRIGASLMRLHFHDCFVQGCDGSVLLNNTDTIESEQDALPNI	97
L78163	TFDASFTDPRIGASLWRLAFHDCFVQGCDGSVLLNNTDTIESEQDALPNI	31
U41657	IRSVSKKDPRMLASLVRLHFHDCFVQGCDASVLLNKTDTVVSEQDAFPNR	98
X90693	LTNVSKTDPRMLASLVRLHFHDCFVLGCDASVLLNNTATIVSEQQAFPNN	97
X90694	LTNVSKTDPRMLASLVRLHFHDCFVLGCDASVLLNNTATIVSEQQAFPNN	90
L36156	LTNVSQSDPRMLGSLIRLHFHDCFVQGCDASILLNDTATIVSEQSAPPNN	96
X90692	***** *** *** ** * * * * * * * * * * *	
L78163	NSIRGLDVVNDIKTAVENSCPDTVSCADILAIAAEIASVLGGGPGWPVPL	147
U41657	NSIRGLDVVNDIKTAVENSCPDTVSCADILAIAAEIASVAGRRSGWPVPL	81
X90693	NSLRGLDVVNQIKTAVEKACPNTVSCADILALSAELSSTLADGPDWKVPL	148
X90694	NSLRGLDVVNQIKLAVEVPCPNTVSCADILALAAQASSVLAQGPSWTVPL	147
L36156	NSLRGLDVVNQIKTAVESACPNTVSCADILALA-QASSVLAQGPSWTVPL	139
X90692	NSIRGLDVINQIKTAVENACPNTVSCADILALSAEISSDLANGPTWQVPL	146
	.**.*.*.*.**	
L78163	GRRDSLTANRTLANQNLPAPFFNLTQLKASFAVQGLNTLDLVTLSGGHTF	197
U41657	GRRDSLTANRTLANQNLPAPFFNLTQLKASFAVQGLNTLDLVTLSGGHTS	131
X90693	GRRDGLTANQLLANQNLPAPFNTTDQLKAAFAAQGLDTTDLVALSGAHTF	198
X90694	GRRDGLTANRTLANQNLPAPFNSLDQLKAAFTAQGLNTTDLVALSGAHTF	197
L36156	GRRDGLTANRTLANQNLPAPFNSLDHLKLHLTAQGLITPVLVALSGAHTF	189
X90692	GRRDSLTANNSLAAQNLPAPTFNLTRLKSNFDNQNLSTTDLVALSGGHTI	196
	***** **** ** ****** * * * . *	
L78163	GRARCSTFINRLYNFSNTGNPDPTLNTTYLEVLRARCPQNATGDNLTNLD	247
U41657	GRARCSTFINRLYNFSNTGLIHLDTTYLEVLRARCPQNATGDNLTNLD	179
X90693	GRAHCSLFVSRLYNFSGTGSPDPTLNTTYLQQLRTICPNGGPGTNLTNFD	248
X90694	GRAHCAQFVSRLYNFSSTGSPDPTLNTTYLQQLRTICPNGGPGTNLTNFD	247
L36156	GRAHCAQFVSRLYNFSSTGSPDPTLNTTYLQQLRTICPNGGPGTNLTNFD	239
X90692	GRGQCRFFVDRLYNFSNTGNPDSTLNTTYLQTLQAICPNGGPGTNLTDLD	246
	.* *.**** * *.****.**	
L78163	LSTPDQFDNRYYSNLLQLNGLLQSDQELFSTPGADTIPIVNSFSSNQNTF	297
U41657	LSTPDQFDNRYYSNLLQLNGLLQSDQERFSTPGADTIPLSIA-SANQNTF	228
X90693	PTTPDKFDKNYYSNLQVKKGLLQSDQELFSTSGSDTISIVNKFATDQKAF	298
X90694	PTTPDKFDKNYYSNLQVKKGLLQSDQELFSTSGADTISIVNKFSTDQNAF	297
L36156	PTTPDKFDKNYYSNLQVKKGLLQSDQELFSTSGADTISIVDKFSTDQNAF	289
X90692	PTTPDTFDSNYYSNLQVGKGLFQSDQELFSRNGSDTISIVNSFANNQTLF	296
	*** ** ** ** ** ** * * * * * * * * * * *	
L78163	FSNFRVSMIKMGNIGVLTGDEGEIRLQCNFVNGDSFGLASVAS-K	341
U41657	FSNFRVSMIKMGNIGVLTGDEGEIRLQCNFVNGDSFGLASVAS-K	272
X90693	FESFRAAMIKMGNIGVLTGNQGEIRKQCNFVNSKSAELGLINVAS-A	344
X90694	FESFKAAMIKMGNIGVLTGTKGEIRKQCNFVNFVNSNSAELDLATIASIV	347
L36156	FESFKAAMIKMGNIGVLTGTKGEIRKQCNFVNSNSAELDLATIASIV	336

X90692		IGVLTGSQGEIRTQCNAVN	GNSSGLATVVT-K	340
L78163 U41657 X90693 X90694 L36156 X90692	DAKQKLVAQSK DAKQKLVAQSK DSSEEGMVSSM ESLEDGIASVI ESLEDGIASVI ESSEDGMASSF	352 283 355 358 347 351		

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